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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTQ_spool/US09765034/runat_05122002_132014_21371/app_query.fasta_1.519
-DB-Pending_Patents_NA_New -QPMT-fastap -SUFFIX=p2n.rnpn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UITS=bits -START=1 -END=-1 -MARTL*=blosum62
-TRANS-human40.cdi -LIST=45 -DOCALICN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09765034_@CGN_1_1_38 @runat_05122002_132014_21371
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Fgapop 6.0,
Delop 6.0,
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/cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
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US-10-278-141-10

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Sequence 1352, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 10, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 17, Appli
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e 1, Appl e 33307, e 33307, e 33307, e 33306, a 33308, e 33308, e 1561, e 1652, a ppl e 17, Appl e 27, Appl e 27, Appl e 21, Appl	Sequence 17, Appl Sequence 21, Appl Sequence 21, Appl

## ALIGNMENTS

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RESULT 1
US-10-72-983-35

Sequence 35, Application US/10272983

GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Chen, Ruoping
APPLICANT: Liaw, Chen W.
APPLICANT: Lia, I-lia

TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
FILE REFERENCE: ARENO050
CURRENT APPLICATION NUMBER: US/10/272,983
CURRENT FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR APPLICATION NUMBER: 60/123,946
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR APPLICATION NUMBER: 60/136,436
PRIOR APPLICATION NUMBER: 60/136,437
PRIOR APPLICATION NUMBER: 60/136,439
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/136,567
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EQ ID NO LENGTH:

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Alignment Scores:
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             PheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGln
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TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PATENTIN Ver. 3.1
SEQ ID NO 1352
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; TYPE: DNA
; ORGANISM: Homo :
US-10-264-237-1352
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GENERAL INFORMATION:
APPLICANT: Birse et
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Conservative:
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DB:
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Pred. No.:
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; ORGANISM: Homo
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                                                              Percent Similarity:
Best Local Similarity:
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                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/908,593
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 08/781,456
PRIOR FILING DATE: 1997-01-10
PRIOR APPLICATION NUMBER: US 60/009,902
PRIOR FILING DATE: 1996-01-11
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
                                                                                                                                                SEQ
                                                                                                                                                                                                                                                              Sequence 1, Applicat GENERAL INFORMATION:
                                                                                                                                                                                                                      APPLICANT: Li, Yi
TITLE OF INVENTION: Human G-Protein Coupl
FILE REFERENCE: PF217C2
CURRENT APPLICATION NUMBER: US/10/270,857
CURRENT FILING DATE: 2002-10-16
                                                        Local S
y Match:
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    Application

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Matches:
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Mismatches:
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RESULT 4
US-10-270-587-1
; Sequence 1, Application US/1; GENERAL INFORMATION:
; APPLICANY: Li, Yi
; TITLE OF INVENTION: Human G
; FILE REFERENCE: PF217C2
; CURRENT APPLICATION NUMBER:
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CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: US 09/908,593
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 08/781,456
PRIOR FILING DATE: 1997-01-10
PRIOR APPLICATION NUMBER: US 60/009,902
PRIOR FILING DATE: 1996-01-11
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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Best Local Similarity:
Query Match:
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; ORGANISM: HOMO
US-10-270-587-1
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Best Local Similarity:
Query Match:
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TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPL
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLEC
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO000750CON
CURRENT APPLICATION NUMBER: US/10/270,144
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/205,196
PRIOR APPLICATION NUMBER: 60/205,196
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-270-144-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1
LENGTH: 1014
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GENERAL INFORMATION:
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ORGANISM: Human
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                                   GTTATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACT
TyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIleIleLysTyr 126
                                                                                                   SerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAlaAsnGly---:::|||||| :::|||
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Matches:
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Sequence 10, Application US/10278141 GENERAL INFORMATION:
                      APPLICANT: AU-YOUNG, Janice
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0096 USA
CURRENT APPLICATION NUMBER: US/10/278,141
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: 60/208,834
PRIOR PILING DATE: 2000-06-02
PRIOR PILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: PATTERSON, Chandra APPLICANT: LU, Dyung Aina M. APPLICANT: THORNTON, Michael
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ELLIOTT, Vicki S.
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        NUMBER: US01/16285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-765-034-2 (1-334) x US-10-278-141-10 (1-1014).
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PRIOR APPLICATION NUMBER: 60/205,628
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: 60/208,861
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: 60/206,222
PRIOR FILING DATE: 2000-05-22
NUMBER: 60/206,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PERL Program SEQ ID NO 10
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LeuGluLysProLeuAsnLeuValIleMetAlaValValIlePheSerValProPheThr
                                      TATACCACGATT - - - ATCCACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAG
                                                                         TyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAlaLeuPro
                                                                                                                                                      TyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeuPheValMetCysPhePhe
                                                                                                                                                                                             ACCAACAGATCAGCCTGTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGG
                                                                                                                                                                                                                                AspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsnTyrAsnLeuIle
                                                                                                                                                                                                                                                                      TrpValLeuValThrLeuGluLeuLeuProIleLeuProLeuIleAsnProValIleThr 166
                                                                                                                                                                                                                                                                                                                                                    CCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGGTG
                                                                                                                                                                                                                                                                                                                                                                                         ProPheArgGluHisLeuLeuGlnLysLysGluPheAlaIleLeuIleSerLeuAlaIle 146
                                                                                                                                                                                                                                                                                                                                                                                                                                 TATAGCAGCATCCTCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCAC
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APPLICANT: WEI, Ming-Hui et al
TITLE OF INVENTION: ISOLARED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENC
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000750CON
CURRENT APPLICATION NUMBER: US/10/270,144
CURRENT EILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/205,196
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 7
SECTIMARE: FastSEQ for Windows Version 4.0
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Query Match:
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; ORGANISM: Human
US-10-270-144-3
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                  TyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIleIleLysTyr 126
                                                                                                                             TATAGCAGCATCCTCTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCAC
                                                                               AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHisAlaAsnLeu
                                                                                                                                                                                               TACATTTTCAAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGC
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Percent Similarity:
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Query Match:
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                                                                                                Alignment Scores:
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                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/JP00/06265
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: JP 11-259986
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                 LENGTH: 2807
TYPE: DNA
ORGANISM: Homo :
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                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn
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                                                                                                                                                         NAME/KEY: CDS
LOCATION: (264)..(1301)
OTHER INFORMATION:
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                          AGACTAAAGTCTGCACTCAGAAAAGGCCATCCACAGAAGGCAAAGACA 125:
                                                MetLeuMetAsnGlnLeuArg-----HisAsnPheLysSerLeuThr
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; OTHER INFORMATION:
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CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: PCT/JP00/06265
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: JP 11-25986
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.1
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GENERAL INFORMATION:
APPLICANT: Yamanouchi Pharmaceutical Co. Ltd.
APPLICANT: Helix Research Institute
TITLE OF INVENTION: PEPTIDE LEUKOTRIENE RECEPTOR
FILE REFERENCE: Q67335
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TyrAsnLeuIleTyrSerMetCysLeuThrLeu-
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US-10-152-319A-2068

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APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT APPLICATION NUMBER: US 60/292,335
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
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                                                                                                                                                            Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 2221
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 2068
LENGTH: 1922
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GENERAL INFORMATION:
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OR FILING DATE: 2001-07-10
OR APPLICATION NUMBER: US 60/315,047
OR FILING DATE: 2001-08-28
OR APPLICATION NUMBER: US 60/324,928
OR FILING DATE: 2001-09-27
OR APPLICATION NUMBER: US 60/330,867
OR APPLICATION NUMBER: US 60/330,867
OR FILING DATE: 2001-11-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/330,462
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    INFORMATION: Genbank Accession No.
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PheSerArgTrpAlaHisGluLeuLeuLeuSerPheArgGluLys
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US-09-979-603A-17
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SOFTWARE: PatentIn version 3.1
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ORGANISM: Sus
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LOCATION: (14)..(1048)
OTHER INFORMATION:
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AsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspPro
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                                                   TGTGGGGTC---ATATGGATCTTTATT---ATGGCTTCCTCAACAGTACTTCTGAAGAAT 544
                                                                                                                         GCAACTGTTCACCCCTTCCGGCTCCTTCATACCACCAGCATCAAGAACGCCTGGATTCTC
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                                                                                       IleSerLeuAlaIleTrpValLeuValThrLeuGluLeuLeuProIleLeuProLeuIle
                                                                                                                                                           IleIleLysTyrProPheArg---GluHisLeuLeuGlnLysLysGluPheAlaIleLeu 141
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GENERAL INFORMATION:
APPLICANT: Yamanouchi Pharmaceutical Co. Ltd.
APPLICANT: Helix Research Institute
TITLE OF INVENTION: PEPTIDE LEUKOTRIENE RECEPTOR
FILE REFERENCE: Q67335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/979,603
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: PCT/JP00/06265
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Sequence 21, Application US/09979603A
GENERAL INFORMATION:
APPLICANT: Yamanouchi Pharmaceutical Co. Ltd.
APPLICANT: Helix Research Institute
TITLE OF INVENTION: PEPTIDE LEUKOTRIENE RECEPTOR
FILE REFERENCE: Q67335
CURRENT APPLICATION NUMBER: US/09/979,603A
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: PCT/JP00/06265
PRIOR APPLICATION NUMBER: JP 11-259986
PRIOR APPLICATION NUMBER: JP 11-259986
PRIOR FILING DATE: 1999-09-14
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   NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
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OTHER INFORMATION:
US-09-979-603A-21
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LENGTH: 1249
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                                                             ProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrp
                                                                                                CGGGATGCTCAGAGGAAGGCACTGACCACTATCGTCATTGCCATGATCATCTTCCTCCTC
                                                                                                                             AlaLeuProLeuGluLysProLeuAsnLeuValIleMetAlaValValIlePheSerVal
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                                 TGTTTTCTGCCATACCATGCACTTCGGACCATCCACTTGGTC
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; OTHER INFORMATION:
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DB:
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GENERAL INFORMATION:
APPLICANT: Yamanouchi Pharmaceutical Co.
APPLICANT: Helix Research Institute
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SEQ ID NO 21
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PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 24
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CURRENT FILING DATE: 2001-11-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/JP00/06265 PRIOR FILING DATE: 2000-09-13
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TYPE: DNA
ORGANISM: Rattus
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                                                     US-09-765-034-2 (1-334) x US-09-958-805A-1 (1-1451)
                                                                                                               Query Match:
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GENERAL INFORMATION:
APPLICANT: Andrew Finlay Walls; Karen-Jane Palmer; Stev
APPLICANT: Jennifer Ann Cairns; Alan Charles Gough
TITLE OF INVENTION: Protease activated Receptor 2 Variants
FILE REFERENCE: DYOUP0223US
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SEQ ID NO 1
LENGTH: 1451
TYPE: DNA
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CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: PCT/GB00/01455
PRIOR FILING DATE: 2000-04-17
                                                                                                                                                                                                                                                                    OTHER INFORMATION: human
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21 LeuGluLysTyrTyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGly 40 :::||| ||| ||| ||| |||||||||:::
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                                                                                                                                                                                                                                                                            1162 ATCGACCCCTTTGTCTATTACTTTGTTTCACATGATTTCAGGGATCATGCAAAGAACGCT 1221
                                                                                                                                                                                                                                                                                                                                                                      1102 CAGAGCCATGTCTATGCCCTGTACATTGTAGCCCTCTGCCTCTACCCCTTAACAGCTGC 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1009 CTCATTGTCACTGTCCTGGCCATGTACCTGATCTGCTTCACTCCTAGTAACCTTCTGCTT 1068
                                                                                                                                 312 HisAsnPheLysSerLeuThrSerPheSerArgTrpAlaHis-----GluLeuLeuLeu 329
                                                                                                                                                                                                                                                                                                                                                                                                               270 GlnValValIleAsnSerPheTyrIleValThrArgProLeuAlaPheLeuAsnSerVal 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 AsnValArg------IleAlaSerArgLeuGlySerTrpLysGlnTyrGlnCysThr 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           889 ATTGGGGTCTTTCTGTTCCCAGGCCTTCCTCACAGGCCTCTGCCTATGTGCTGATGATCAGA 948
                                             330 SerPhe 331
                                                                                                                                                                                                                                   310 Leu-----
                                                                                                                                                                                                                                                                                                                         290 IleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAspMetLeuMetAsnGln 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 LeuValIleMetAlaValValIlePheSerValProPheThrProTyrHisValMetArg 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   949 ATGCTGCGATCTTCTGCCATGGATGAAAACTCAGAGAAGAAAAGGAAGAGGGCCATCAAA 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 PheLeuLysGlnArgAsnArgGlnValAlaThrAlaLeuProLeuGluLysProLeuAsn 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 LeuLeuGlyPheLeuIleProLeuPheValMetCysPhePheTyrTyrLysIleAlaLeu 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 SerGlyAspProAsnTyrAsnLeuIle------TyrSerMetCysLeuThr 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 LeuIleAsnProValIleThrAsp-----AsnGlyThrThrCysAsnAspPheAlaSer 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 IleLeuIleSerLeuAlaIleTrpValLeuValThrLeuGluLeuLeuProIleLeuPro 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 ArgTyrLeuIleIleLysTyrProPheArgGluHisLeuLeuGlnLysLysGluPheAla 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      544 GCCTATCACATACATGCCAACAACTGGATTTATGGGGAAGCTCTTTGTAATGTGCTTATT 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424 AACGGCATGGCCCTGTGGGTCTTTCTTTTCCGAACTAAGAAGAAGCACCCTGCTGTGATT 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  664 AGGTATTGGGTCATCGTGAACCCCATG---GGGCACTCCAGGAAGAAGGCAAACATTGCC 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 CTGACCACGGTCTTCCTTCCAATTGTCTACACAATTGTGTTTGTGGTGGGTTTGCCAAGT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 ArgSerTyrAlaAsn---GlyAsnTrpIleTyrGlyAspValLeuCysIleSerAsnArg 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 AsnThrIleValValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIle 60
                                                                                        CACTCCAGGAAATCCAGCTCTTA-CTCTTCAAGTTCAACCACTGTTAAGACCTCCTATTG 1340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGAAGCAGACCATCTTCATTCCTGCCCTGAACATCACGACCTGTCATGATGTTTTG--- 837
                                                                                                                                                                                                                                -----Arg 311
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